

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/560,491
Source: IFWP
Date Processed by STIC: 12/21/2005

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 12/21/2005

PATENT APPLICATION: US/10/560,491

TIME: 15:20:11

Input Set : N:\RJAVED\10560491.txt

Output Set: N:\CRF4\12212005\J560491.raw

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3 <110> APPLICANT: YANASE, Michiyo
4     TAKATA, Hiroki
5     FUJII, Kazutoshi
6     TAKAHA, Takeshi
7     Kuriki, Takashi
9 <120> TITLE OF INVENTION: A METHOD FOR IMPROVING THE THERMOSTABILITY OF ALPHA-GLUCAN
PHOSPHORYLASE
10     (GP)
12 <130> FILE REFERENCE: EG012PCT
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/560,491
C--> 15 <141> CURRENT FILING DATE: 2005-12-12
17 <150> PRIOR APPLICATION NUMBER: JP 2003-173972
18 <151> PRIOR FILING DATE: 2003-06-18
20 <160> NUMBER OF SEQ ID NOS: 48
22 <170> SOFTWARE: PatentIn version 3.3
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 3101
26 <212> TYPE: DNA
27 <213> ORGANISM: Solanum tuberosum
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31 <221> NAME/KEY: CDS
32 <222> LOCATION: (44)..(2941)
34 <220> FEATURE:
35 <221> NAME/KEY: mat_peptide
36 <222> LOCATION: (194)..(2941)
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40                                     Met Ala Thr Ala
41                                     -50
43 aat gga gca cac ttg ttc aac cat tac agc tcc aat tcc aga ttc atc      103
44 Asn Gly Ala His Leu Phe Asn His Tyr Ser Ser Asn Ser Arg Phe Ile
45   -45                -40                -35
47 cat ttc act tct aga aac aca agc tcc aaa ttg ttc ctt acc aaa acc      151
48 His Phe Thr Ser Arg Asn Thr Ser Ser Lys Leu Phe Leu Thr Lys Thr
49 -30                -25                -20                -15
51 tcc cat ttt cgg aga ccc aaa cgc tgt ttc cat gtc aac aat acc ttg      199
52 Ser His Phe Arg Arg Pro Lys Arg Cys Phe His Val Asn Asn Thr Leu
53   -10                -5                -1  1
55 agt gag aaa att cac cat ccc att act gaa caa ggt ggt gag agc gac      247
56 Ser Glu Lys Ile His His Pro Ile Thr Glu Gln Gly Gly Glu Ser Asp
57   5                10                15
59 ctg agt tct ttt gct cct gat gcc gca tct att acc tca agt atc aaa      295
60 Leu Ser Ser Phe Ala Pro Asp Ala Ala Ser Ile Thr Ser Ser Ile Lys
61   20                25                30

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63 tac cat gca gaa ttc aca cct gta ttc tct cct gaa agg ttt gag ctc 343
64 Tyr His Ala Glu Phe Thr Pro Val Phe Ser Pro Glu Arg Phe Glu Leu
65 35 40 45 50
67 cct aag gca ttc ttt gca aca gct caa agt gtt cgt gat tcg ctc ctt 391
68 Pro Lys Ala Phe Phe Ala Thr Ala Gln Ser Val Arg Asp Ser Leu Leu
69 55 60 65
71 att aat tgg aat gct acg tat gat att tat gaa aag ctg aac atg aag 439
72 Ile Asn Trp Asn Ala Thr Tyr Asp Ile Tyr Glu Lys Leu Asn Met Lys
73 70 75 80
75 caa gcg tac tat cta tcc atg gaa ttt ctg cag ggt aga gca ttg tta 487
76 Gln Ala Tyr Tyr Leu Ser Met Glu Phe Leu Gln Gly Arg Ala Leu Leu
77 85 90 95
79 aat gca att ggt aat ctg gag ctt act ggt gca ttt gcg gaa gct ttg 535
80 Asn Ala Ile Gly Asn Leu Glu Leu Thr Gly Ala Phe Ala Glu Ala Leu
81 100 105 110
83 aaa aac ctt ggc cac aat cta gaa aat gtg gct tct cag gaa cca gat 583
84 Lys Asn Leu Gly His Asn Leu Glu Asn Val Ala Ser Gln Glu Pro Asp
85 115 120 125 130
87 gct gct ctt gga aat ggg ggt ttg gga cgg ctt gct tcc tgt ttt ctg 631
88 Ala Ala Leu Gly Asn Gly Gly Leu Gly Arg Leu Ala Ser Cys Phe Leu
89 135 140 145
91 gac tct ttg gca aca cta aac tac cca gca tgg ggc tat gga ctt agg 679
92 Asp Ser Leu Ala Thr Leu Asn Tyr Pro Ala Trp Gly Tyr Gly Leu Arg
93 150 155 160
95 tac aag tat ggt tta ttt aag caa cgg att aca aaa gat ggt cag gag 727
96 Tyr Lys Tyr Gly Leu Phe Lys Gln Arg Ile Thr Lys Asp Gly Gln Glu
97 165 170 175
99 gag gtg gct gaa gat tgg ctt gaa att ggc agt cca tgg gaa gtt gtg 775
100 Glu Val Ala Glu Asp Trp Leu Glu Ile Gly Ser Pro Trp Glu Val Val
101 180 185 190
103 agg aat gat gtt tca tat cct atc aaa ttc tat gga aaa gtc tct aca 823
104 Arg Asn Asp Val Ser Tyr Pro Ile Lys Phe Tyr Gly Lys Val Ser Thr
105 195 200 205 210
107 gga tca gat gga aag agg tat tgg att ggt gga gag gat ata aag gca 871
108 Gly Ser Asp Gly Lys Arg Tyr Trp Ile Gly Gly Glu Asp Ile Lys Ala
109 215 220 225
111 gtt gcg tat gat gtt ccc ata cca ggg tat aag acc aga acc aca atc 919
112 Val Ala Tyr Asp Val Pro Ile Pro Gly Tyr Lys Thr Arg Thr Thr Ile
113 230 235 240
115 agc ctt cga ctg tgg tct aca cag gtt cca tca gcg gat ttt gat tta 967
116 Ser Leu Arg Leu Trp Ser Thr Gln Val Pro Ser Ala Asp Phe Asp Leu
117 245 250 255
119 tct gct ttc aat gct gga gag cac acc aaa gca tgt gaa gcc caa gca 1015
120 Ser Ala Phe Asn Ala Gly Glu His Thr Lys Ala Cys Glu Ala Gln Ala
121 260 265 270
123 aac gct gag aag ata tgt tac ata ctc tac cct ggg gat gaa tca gag 1063
124 Asn Ala Glu Lys Ile Cys Tyr Ile Leu Tyr Pro Gly Asp Glu Ser Glu
125 275 280 285 290
127 gag gga aag atc ctt cgg ttg aag caa caa tat acc tta tgc tcg gct 1111

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128	Glu	Gly	Lys	Ile	Leu	Arg	Leu	Lys	Gln	Gln	Tyr	Thr	Leu	Cys	Ser	Ala	
129					295					300					305		
131	tct	ctc	caa	gat	att	att	tct	cga	ttt	gag	agg	aga	tca	ggt	gat	cgt	1159
132	Ser	Leu	Gln	Asp	Ile	Ile	Ser	Arg	Phe	Glu	Arg	Arg	Ser	Gly	Asp	Arg	
133				310					315					320			
135	att	aag	tgg	gaa	gag	ttt	cct	gaa	aaa	gtt	gct	gtg	cag	atg	aat	gac	1207
136	Ile	Lys	Trp	Glu	Glu	Phe	Pro	Glu	Lys	Val	Ala	Val	Gln	Met	Asn	Asp	
137			325					330					335				
139	act	cac	cct	aca	ctt	tgt	atc	cct	gag	ctg	atg	aga	ata	ttg	ata	gat	1255
140	Thr	His	Pro	Thr	Leu	Cys	Ile	Pro	Glu	Leu	Met	Arg	Ile	Leu	Ile	Asp	
141		340					345					350					
143	ctg	aag	ggc	ttg	aat	tgg	aat	gaa	gct	tgg	aat	att	act	caa	aga	act	1303
144	Leu	Lys	Gly	Leu	Asn	Trp	Asn	Glu	Ala	Trp	Asn	Ile	Thr	Gln	Arg	Thr	
145	355					360				365					370		
147	gtg	gcc	tac	aca	aac	cat	act	gtt	ttg	cct	gag	gca	ctg	gag	aaa	tgg	1351
148	Val	Ala	Tyr	Thr	Asn	His	Thr	Val	Leu	Pro	Glu	Ala	Leu	Glu	Lys	Trp	
149				375					380				385				
151	agt	tat	gaa	ttg	atg	cag	aaa	ctc	ctt	ccc	aga	cat	gtc	gaa	atc	att	1399
152	Ser	Tyr	Glu	Leu	Met	Gln	Lys	Leu	Leu	Pro	Arg	His	Val	Glu	Ile	Ile	
153			390					395					400				
155	gag	gcg	att	gac	gag	gag	ctg	gta	cat	gaa	att	gta	tta	aaa	tat	ggt	1447
156	Glu	Ala	Ile	Asp	Glu	Glu	Leu	Val	His	Glu	Ile	Val	Leu	Lys	Tyr	Gly	
157		405					410					415					
159	tca	atg	gat	ctg	aac	aaa	ttg	gag	gaa	aag	ttg	act	aca	atg	aga	atc	1495
160	Ser	Met	Asp	Leu	Asn	Lys	Leu	Glu	Glu	Lys	Leu	Thr	Thr	Met	Arg	Ile	
161		420				425					430						
163	tta	gaa	aat	ttt	gat	ctt	ccc	agt	tct	gtt	gct	gaa	tta	ttt	att	aag	1543
164	Leu	Glu	Asn	Phe	Asp	Leu	Pro	Ser	Ser	Val	Ala	Glu	Leu	Phe	Ile	Lys	
165	435				440					445					450		
167	cct	gaa	atc	tca	gtt	gat	gat	gat	act	gaa	aca	gta	gaa	gtc	cat	gac	1591
168	Pro	Glu	Ile	Ser	Val	Asp	Asp	Asp	Thr	Glu	Thr	Val	Glu	Val	His	Asp	
169				455				460					465				
171	aaa	gtt	gaa	gct	tcc	gat	aaa	gtt	gtg	act	aat	gat	gaa	gat	gac	act	1639
172	Lys	Val	Glu	Ala	Ser	Asp	Lys	Val	Val	Thr	Asn	Asp	Glu	Asp	Asp	Thr	
173			470					475					480				
175	ggt	aag	aaa	act	agt	gtg	aag	ata	gaa	gca	gct	gca	gaa	aaa	gac	att	1687
176	Gly	Lys	Lys	Thr	Ser	Val	Lys	Ile	Glu	Ala	Ala	Ala	Glu	Lys	Asp	Ile	
177		485					490					495					
179	gac	aag	aaa	act	ccc	gtg	agt	ccg	gaa	cca	gct	gtt	ata	cca	cct	aag	1735
180	Asp	Lys	Lys	Thr	Pro	Val	Ser	Pro	Glu	Pro	Ala	Val	Ile	Pro	Pro	Lys	
181		500				505					510						
183	aag	gta	cgc	atg	gcc	aac	ttg	tgt	gtt	gtg	ggc	ggc	cat	gct	gtt	aat	1783
184	Lys	Val	Arg	Met	Ala	Asn	Leu	Cys	Val	Val	Gly	Gly	His	Ala	Val	Asn	
185	515				520					525					530		
187	gga	gtt	gct	gag	atc	cat	agt	gaa	att	gtg	aag	gag	gag	gtt	ttc	aat	1831
188	Gly	Val	Ala	Glu	Ile	His	Ser	Glu	Ile	Val	Lys	Glu	Glu	Val	Phe	Asn	
189				535				540					545				
191	gac	ttc	tat	gag	ctc	tgg	ccg	gaa	aag	ttc	caa	aac	aaa	aca	aat	gga	1879
192	Asp	Phe	Tyr	Glu	Leu	Trp	Pro	Glu	Lys	Phe	Gln	Asn	Lys	Thr	Asn	Gly	

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193		550		555		560		
195	gtg act cca	aga aga tgg att cgt	ttc tgc aat cct cct	ctt agt gcc	1927			
196	Val Thr Pro	Arg Arg Trp Ile Arg	Phe Cys Asn Pro Pro	Leu Ser Ala				
197		565		570		575		
199	atc ata act	aag tgg act ggt	aca gag gat tgg	gtc ctg aaa act	gaa	1975		
200	Ile Ile Thr	Lys Trp Thr Gly	Thr Glu Asp Trp Val	Leu Lys Thr Glu				
201		580		585		590		
203	aag ttg gca	gaa ttg cag aag	ttt gct gat aat	gaa gat ctt	caa aat	2023		
204	Lys Leu Ala	Glu Leu Gln Lys	Phe Ala Asp Asn	Glu Asp Leu	Gln Asn			
205	595		600		605		610	
207	gag tgg agg	gaa gca aaa agg	agc aac aag att	aaa gtt gtc	tcc ttt	2071		
208	Glu Trp Arg	Glu Ala Lys Arg	Ser Asn Lys Ile	Lys Val Val	Ser Phe			
209		615		620		625		
211	ctc aaa gaa	aag aca ggg tat	tct gtt gtc cca	gat gca atg	ttt gat	2119		
212	Leu Lys Glu	Lys Thr Gly Tyr	Ser Val Val Pro	Asp Ala Met	Phe Asp			
213		630		635		640		
215	att cag gta	aaa cgc att cat	gag tac aag cga	caa ctg tta	aat atc	2167		
216	Ile Gln Val	Lys Arg Ile His	Glu Tyr Lys Arg	Gln Leu Leu	Asn Ile			
217		645		650		655		
219	ttc ggc atc	gtt tat cgg tat	aag aag atg aaa	gaa atg aca	gct gca	2215		
220	Phe Gly Ile	Val Tyr Arg Tyr	Lys Lys Met Lys	Glu Met Thr	Ala Ala			
221		660		665		670		
223	gaa aga aag	act aac ttc gtt	cct cga gta tgc	ata ttt ggg	gga aaa	2263		
224	Glu Arg Lys	Thr Asn Phe Val	Pro Arg Val Cys	Ile Phe Gly	Gly Lys			
225	675		680		685		690	
227	gct ttt gcc	aca tat gtg caa	gcc aag agg att	gta aaa ttt	atc aca	2311		
228	Ala Phe Ala	Thr Tyr Val Gln	Ala Lys Arg Ile	Val Lys Phe	Ile Thr			
229		695		700		705		
231	gat gtt ggt	gct act ata aat	cat gat cca	gaa atc ggt	gat ctg	ttg	2359	
232	Asp Val Gly	Ala Thr Ile Asn	His Asp Pro Glu	Ile Gly Asp	Leu Leu			
233		710		715		720		
235	aag gta gtc	ttt gtg cca gat	tac aat gtc agt	gtt gct gaa	ttg cta	2407		
236	Lys Val Val	Phe Val Pro Asp	Tyr Asn Val Ser	Val Ala Glu	Leu Leu			
237		725		730		735		
239	att cct gct	agc gat cta tca	gaa cat atc agt	acg gct gga	atg gag	2455		
240	Ile Pro Ala	Ser Asp Leu Ser	Glu His Ile Ser	Thr Ala Gly	Met Glu			
241		740		745		750		
243	gcc agt gga	acc agt aat atg	aag ttt gca atg	aat ggt tgt	atc caa	2503		
244	Ala Ser Gly	Thr Ser Asn Met	Lys Phe Ala Met	Asn Gly Cys	Ile Gln			
245	755		760		765		770	
247	att ggt aca	ttg gat ggc gct	aat gtt gaa ata	agg gaa gag	gtt gga	2551		
248	Ile Gly Thr	Leu Asp Gly Ala	Asn Val Glu Ile	Arg Glu Glu	Val Gly			
249		775		780		785		
251	gaa gaa aac	ttc ttt ctc ttt	ggt gct caa gct	cat gaa att	gca ggg	2599		
252	Glu Glu Asn	Phe Phe Leu Phe	Gly Ala Gln Ala	His Glu Ile	Ala Gly			
253		790		795		800		
255	ctt aga aaa	gaa aga gct gac	gga aag ttt gta	cct gat gaa	cgt ttt	2647		
256	Leu Arg Lys	Glu Arg Ala Asp	Gly Lys Phe Val	Pro Asp Glu	Arg Phe			
257		805		810		815		

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259 gaa gag gtg aag gaa ttt gtt aga agc ggt gct ttt ggc tct tat aac      2695
260 Glu Glu Val Lys Glu Phe Val Arg Ser Gly Ala Phe Gly Ser Tyr Asn
261      820      825      830
263 tat gat gac cta att gga tcg ttg gaa gga aat gaa ggt ttt ggc cgt      2743
264 Tyr Asp Asp Leu Ile Gly Ser Leu Glu Gly Asn Glu Gly Phe Gly Arg
265 835      840      845      850
267 gct gac tat ttc ctt gtg ggc aag gac ttc ccc agt tac ata gaa tgc      2791
268 Ala Asp Tyr Phe Leu Val Gly Lys Asp Phe Pro Ser Tyr Ile Glu Cys
269      855      860      865
271 caa gag aaa gtt gat gag gca tat cgc gac cag aaa agg tgg aca acg      2839
272 Gln Glu Lys Val Asp Glu Ala Tyr Arg Asp Gln Lys Arg Trp Thr Thr
273      870      875      880
275 atg tca atc ttg aat aca gcg gga tcg tac aag ttc agc agt gac aga      2887
276 Met Ser Ile Leu Asn Thr Ala Gly Ser Tyr Lys Phe Ser Ser Asp Arg
277      885      890      895
279 aca atc cat gaa tat gcc aaa gac att tgg aac att gaa gct gtg gaa      2935
280 Thr Ile His Glu Tyr Ala Lys Asp Ile Trp Asn Ile Glu Ala Val Glu
281      900      905      910
283 ata gca taagaggggg aagtgaatga aaaataacaa aggcacagta agtagtttct      2991
284 Ile Ala
285 915
287 ctttttatca tgtgatgaag gtatataatg tatgtgtaag aggatgatgt tattaccaca      3051
289 taataagaga tgaagagtct cattttgctt caaaaaaaaaa aaaaaaaaaa      3101
292 <210> SEQ ID NO: 2
293 <211> LENGTH: 966
294 <212> TYPE: PRT
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304      -30      -25      -20
307 Leu Thr Lys Thr Ser His Phe Arg Arg Pro Lys Arg Cys Phe His Val
308      -15      -10      -5
311 Asn Asn Thr Leu Ser Glu Lys Ile His His Pro Ile Thr Glu Gln Gly
312 -1 1      5      10
315 Gly Glu Ser Asp Leu Ser Ser Phe Ala Pro Asp Ala Ala Ser Ile Thr
316 15      20      25      30
319 Ser Ser Ile Lys Tyr His Ala Glu Phe Thr Pro Val Phe Ser Pro Glu
320      35      40      45
323 Arg Phe Glu Leu Pro Lys Ala Phe Phe Ala Thr Ala Gln Ser Val Arg
324      50      55      60
327 Asp Ser Leu Leu Ile Asn Trp Asn Ala Thr Tyr Asp Ile Tyr Glu Lys
328      65      70      75
331 Leu Asn Met Lys Gln Ala Tyr Tyr Leu Ser Met Glu Phe Leu Gln Gly
332      80      85      90
335 Arg Ala Leu Leu Asn Ala Ile Gly Asn Leu Glu Leu Thr Gly Ala Phe
336 95      100      105      110
339 Ala Glu Ala Leu Lys Asn Leu Gly His Asn Leu Glu Asn Val Ala Ser

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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 9

VERIFICATION SUMMARY

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Input Set : **N:\RJAVED\10560491.txt**

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L:14 M:270 C: Current Application Number differs, Replaced Current Application Number

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date